

[illegible]

(1) GENERAL INFORMATION:

(i) APPLICANT: Bendele, Alison M.
Sennello, Regina M.
Edwards, Carl K.

(ii) TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING PROTEIN FOR TREATING TNF-MEDIATED DISEASES

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 DeHavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: NOT YET KNOWN
(B) FILING DATE: 08-DEC-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,587
(B) FILING DATE: 06-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/036,355
(B) FILING DATE: 23-JAN-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/039,315
(B) FILING DATE: 07-FEB-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/052,023
(B) FILING DATE: 09-JUL-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Zindrick, Thomas K.
(B) REGISTRATION NUMBER: 32,185
(C) REFERENCE/DOCKET NUMBER: A-430D

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAT	AGT	GTG	TGT	CCC	CAA	GGA	AAA	TAT	ATC	CAC	CCT	CAA	AAT	AAT	TCG	48
Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	
1				5				10					15			
ATT	TGC	TGT	ACC	AAG	TGC	CAC	AAA	GGA	ACC	TAC	TTG	TAC	AAT	GAC	TGT	96
Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	
			20					25					30			
CCA	GGC	CCG	GGG	CAG	GAT	ACG	GAC	TGC	AGG	GAG	TGT	GAG	AGC	GGC	TCC	144
Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	
		35					40					45				
TTC	ACC	GCT	TCA	GAA	AAC	CAC	CTC	AGA	CAC	TGC	CTC	AGC	TGC	TCC	AAA	192
Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	
		50				55				60						
TGC	CGA	AAG	GAA	ATG	GGT	CAG	GTG	GAG	ATC	TCT	TCT	TGC	ACA	GTG	GAC	240
Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	
65				70				75					80			
CGG	GAC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG	288
Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	
			85				90						95			
AGT	GAA	AAC	CTT	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	336
Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	
			100				105					110				
ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	384
Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	
			115				120					125				
CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC	432
His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	
		130				135					140					

AAT	483
Asn	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTG CCC GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC	48
Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser	
1 5 10 15	
ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC	96
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys	
20 25 30	
AGC AAG TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC	144
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr	
35 40 45	
TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC	192
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu	
50 55 60	
TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT	240
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser	
65 70 75 80	
GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC	288
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys	
85 90 95	
ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC	336
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys	
100 105 110	
CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC	384
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala	
115 120 125	
AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG	432
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro	
130 135 140	
GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC	480
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His	
145 150 155 160	

CCC AGC CCC CCA GCT GAA GGG AGC ACT GGC GAC 705
Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230 235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser
1				5					10					15	
Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys
			20					25					30		
Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys	Thr	Lys	Thr
		35					40					45			
Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	Thr	Gln	Leu
	50					55					60				
Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys	Ser	Ser
65					70					75					80
Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg	Ile	Cys
				85					90					95	
Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys
			100					105					110		
Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala
		115					120					125			

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